

AMENDMENTS

In the Specification

At page 12, lines 2-4, please delete "Non-limiting examples of these programs are Blast¹, Fasta², DNA Star, MegAlign, and GeneJockey." and the accompanying footnotes, and insert in its place --Non-limiting examples of these programs are Blast (available on the worldwide web at <http://www.ncbi.nlm.nih.gov/BLAST/>), Fasta (Genetics Computing Group package, Madison, Wisconsin), DNA Star, MegAlign, and GeneJockey.--

In the Claims:

Please cancel claims 24-48 without prejudice to future prosecution in this application or a related application.

Please amend claims 1, 2, 3, 17, 18 and 19 as follows:

1. (Amended) An array comprising a plurality of polynucleotide probes immobilized on a solid support, wherein:

(a) the plurality of polynucleotide probes corresponds to a multiplicity of gene transcripts and comprises at least 100 polynucleotides that are each complementary to a distinct gene transcript;

(b) each polynucleotide probe of the plurality is localized to a predetermined region on the solid support;

(c) each polynucleotide probe of the plurality is from about 50 to 500 nucleotides in length;

(d) each polynucleotide probe of the plurality is complementary to 3' untranslated sequence of a gene transcript, said untranslated sequence having a defined chromosomal location.

2. (Amended) An array of claim 1, wherein each polynucleotide probe of the plurality of polynucleotide probes is from about 50 to 400 nucleotides in length.